AMENDMENTS TO CLAIMS

This listing of the claims replaces all prior versions and listings:

1. (currently amended): A method for identifying a gene; wherein the method comprises:

(a) obtaining a putative gene sequence (PGS), wherein the putative gene sequence is not identified as a gene;

(b) contacting a cell with an exogenous molecule, wherein the cell comprises the putative gene sequence, and wherein the exogenous molecule binds to and modulates expression of the putative gene sequence; and

(c) assaying the cell for at least one selected phenotype;

wherein, if one or more of the selected phenotypes are observed, the putative gene sequence is identified as a gene.

2. (original): The method of claim 1, wherein the gene encodes a protein.

3. (original): The method of claim 1, wherein the gene encodes a RNA selected from the group consisting of structural RNA, regulatory RNA, enzymatic RNA, antisense RNA, ribozyme, ribosomal RNA and transfer RNA.

4. (original): The method of claim 1,wherein the exogenous molecule is a zinc finger protein.

5. (original): The method of claim 1, wherein the exogenous molecule binds near the putative transcription startsite of the PGS.

6. (original): The method of claim 1, wherein the exogenous molecule binds in the putative transcribed region of the PGS.

7. (original): The method of claim 6, wherein the exogenous molecule binds in the putative coding region of the PGS.

8. (original): The method of claim 1, wherein the exogenous molecule binds in a putative nontranscribed regulatory region of the PGS.

9. (original): The method of claim 1, wherein the exogenous molecule comprises an activation domain.

10. (original): The method of claim 9, wherein the activation domain is selected from the group consisting of VP16, p65 and functional fragments thereof.

11. (original): The method of claim 1, wherein the exogenous molecule comprises a repression domain.

12. (original): The method of claim 11, wherein the repression domain is selected from the group consisting of KRAB, v-erbA and functional fragments thereof.

13. (original): The method of claim 1, wherein the exogenous molecule comprises a bifunctional domain (BFD), wherein the activity of the bifunctional domain is dependent upon interaction of the BFD with a second molecule.

14. (original): The method of claim 13, wherein the BFD is selected from the group consisting of thyroid hormone receptor, retinoic acid receptor, estrogen receptor, glucocorticoid receptor and functional fragments thereof.

15. (withdrawn): The method of claim 13, wherein the second molecule is a protein.

16. (original): The method of claim 13, wherein the second molecule is a small molecule.

17. (original): The method of claim 16, wherein the small molecule is selected from the group consisting of 3,5,3'-triiodo-L-thyronine (T3), all-*trans*- retinoic acid, estradiol, tamoxifen, 4-hydroxy-tamoxifen, RU-486 and dexamethasone.

18. (original): The method of claim 1, wherein the cell is an animal cell.

19. (original): The method of claim 18 wherein the cell is a human cell.

20. (withdrawn): The method of claim 1, wherein the cell is a plant cell.

21. (withdrawn): The method of claim 1, wherein the cell is a fungal cell.

22. (withdrawn): The method of claim 1, wherein the cell is a bacterial cell.

23. (withdrawn): The method of claim 1, wherein the phenotype is a change in a property selected from the group consisting of cell growth, cell cycle control, cellular physiology and cellular response to a pathogen.

24. (original): The method of claim 1, wherein the phenotype is expression of a RNA molecule.

25. (withdrawn): The method of claim 1, wherein the phenotype is an alteration in the transcriptional program of the cell.

26. (original): The method of claim 1, wherein the cell is infected with a virus.

27. (original): The method of claim 26, wherein the gene is a viral gene.

28. (original): The method of claim 1, wherein the putative gene sequence is obtained from a gene prediction algorithm.

29. (original): The method of claim 1, wherein the putative gene sequence is obtained by analysis of expressed sequence tags.

30. (original): The method of claim 1, wherein the putative gene sequence is obtained by homology.